CLAIMS

What is claimed is:

1. A method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid, comprising the steps of:

providing patient sample nucleic acid containing multiple loci at a site;

providing one or more blockers, the blockers being selected for particular loci;

hybridizing the blockers with the patient sample nucleic acid, leaving at least one loci unblocked;

providing at least one discriminator, the discriminator being capable of binding with the at least one unblocked loci;

hybridizing the discriminators with the patient sample; and

detecting the formation of a hyubridization event.

2. The method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 1, further including the step of providing a second blocker set after performing the detecting step.

3. A method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 1, wherein the identity of the loci involved in the hybridization event is determined by selectively blocking the previously unblocked loci.

4. A method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 2, wherein the blockers are changed sequentially at a single site.

5. A method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 2, wherein different blockers are provided to different sites.

6. The method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 1, wherein the site comprises a site of an actively addressable electronic microarray.

7. The method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 6, wherein the addressable electronic microarray includes a permeation layer.

8. The method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 1, wherein the patient sample is amplified.

9. The method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 8, wherein the amplification includes polymerase chain reaction (PCR).

10. The method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 8, wherein the amplification includes ligase chain reaction (LCR).

11. The method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 8, wherein the amplification include strand displacement amplification (SDA).

12. The method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 8, wherein the amplification includes the transcription-based amplification system (TAS).

13. The method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 8, wherein the amplification includes the self-sustained sequence replication system (3SR).

14. The method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 8, wherein the amplification includes the Qβ replicase amplification system (Qβ).

15. The method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 8, wherein multiple amplifications are accomplished in multiplex polymerase-based reactions with specially selected primers for identified loci of genomic nucleic acid containing the known polymorphisms.

16. The method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 1, wherein the discriminator hybridizes with a universal reporter.

17. The method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 1, wherein at least two loci are unblocked.

18. The method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 1, further includes the step of performing a screening step.

19. The method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 1, wherein the patient sample nucleic acid comprises multiple segments containing different loci.

20. The method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 19, wherein the multiple segments containing different loci are affixed to the same site.

21. The method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 19, wherein the multiple segments containing different loci are affixed to the different sites.

22. The method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 6, wherein the multiple patient samples are provided on multiple sites of the microarray.

23. The method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 1, further including amplification controls indicated by different colors.

24. The method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 1, wherein the loci are indicative of genetic diseases.

25. The method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 24, wherein the genetic disease is cystic fibrosis.

26. The method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 24, wherein the genetic disease is selected from the group consisting of Beta-Thalassemia, hereditary hemochromatosis, Gaucher, Tay-Sachs, Nieman-Pick, HIV, and epilepsy.

27. The method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 1, further including a stabilizer adjacent the dsicriminator.

28. A method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid comprising the steps of:

providing a patient sample containing multiple loci,

performing a screening step, comprising providing at least two probes for different loci, and detecting the presence of a hybridization event between the patient sample and the probes,

and, if a hybridization event is detected,

providing a first set of blockers to the loci, the set of blockers comprising a subset of the sites corresponding to the probes, and

providing probes to patient sample, and detecting a hybridization event.

29. The method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 28, wherein in the screening step there are at least three probes for different loci.

30. The method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 28, wherein in the screening step there are at least five probes for different loci.

31. The method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 28, wherein the screening step is performed at one site, and if a hybridization event is detected, multiple sites containing patient sample are subsequently probed.

32. The method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 31, wherein different blocker sets are provided to the different patient samples at the multiple sites.

33. The method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 32, wherein the blocker sets block all but one loci.

34. A method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid comprising the steps of:

loading a patient sample containing multiple loci at multiple sites, including at least a first site and a second site, and

providing a first set of blockers selectively for a subset of the loci to the first site and a second set of blockers, which are different from the first set of blockers, selectively to a different subset of the loci at the second site.

35. The method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 34, wherein there exist unblocked loci.

36. The method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 35, wherein discriminators are provided for detecting the unblocked loci.

37. The method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 34, wherein the multiple sites comprise sites of an actively addressable electronic microarray.

38. The method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 37, wherein the addressable electronic microarray includes a permeation layer.

39. The method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 34, wherein the patient sample is amplified.

40. A method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid, comprising the steps of:

attaching the sample of patient nucleic acid to a test site, the patient sample having multiple identified loci;

providing a blocker set to the patient sample so as to block some, but not all, of the loci; and

providing discriminators for detecting unblocked loci.

41. A system for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid comprising:

loading nucleic acid from the identified loci at an addressable site,

providing mutant discriminator probes comprising oligonucleotides selective for a member of the set of known polymorphisms,

providing a first common nucleotide sequence, and

providing a universal reporter comprising a label and a nucleotide sequence complementary to the first common nucleotide sequence of the mutant discriminator probe.

42. A kit for use in a process of detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid, said kit comprising:

at least one blocker capable of binding with at least one loci contained in the patient sample nucleic acid;

at least one discriminator capable of binding with at least one different loci in the patient sample nucleic acid; and

at least one universal reporter capable of binding with the at least one discriminator.

43. The kit of claim 42, further comprising at least one amplification control being capable of binding with the patient nucleic acid.

44. The kit of claim 43, further comprising an additional universal reporter capable of binding with the at least one amplification control.